



SEQUENCE LISTING

<110> Vander Horn, Peter B.
MJ Bioworks, Inc.

<120> Methods of Making Hybrid Proteins

<130> 020130-001420US

<140> US 10/627,592

<141> 2003-07-25

<150> US 60/463,781

<151> 2003-04-17

<150> US 60/483,287

<151> 2003-06-27

<160> 50

<170> PatentIn Ver. 2.1

<210> 1

<211> 493

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:BlastP
alignment Pyrococcus furiosus DNA polymerase (Pfu)
query sequence

<400> 1

Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
1 5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
20 25 30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
35 40 45

Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
50 55 60

Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
65 70 75 80

Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
85 90 95

Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115 120 125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
 145 150 155 160
 Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
 165 170 175
 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
 180 185 190
 Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
 195 200 205
 Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
 210 215 220
 Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
 225 230 235 240
 Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
 245 250 255
 His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
 260 265 270
 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
 275 280 285
 Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn
 290 295 300
 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
 305 310 315 320
 Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
 325 330 335
 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
 340 345 350
 Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
 355 360 365
 Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser
 370 375 380
 Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
 385 390 395 400
 Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
 405 410 415
 His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr
 420 425 430
 Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
 435 440 445
 Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
 450 455 460

Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu
 465 470 475 480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser
 485 490

<210> 2
 <211> 283
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:BlastP
 alignment Pyrococcus furiosus DNA polymerase (Pfu)
 query sequence

<400> 2
 Asn Ser Phe Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys
 1 5 10 15
 Lys Glu Cys Ala Glu Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu
 20 25 30
 Leu Val Trp Lys Glu Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr
 35 40 45
 Ile Asp Thr Asp Gly Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu
 50 55 60
 Glu Ile Lys Lys Lys Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys
 65 70 75 80
 Leu Pro Gly Leu Leu Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly
 85 90 95
 Phe Phe Val Thr Lys Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys
 100 105 110
 Val Ile Thr Arg Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile
 115 120 125
 Ala Lys Glu Thr Gln Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly
 130 135 140
 Asp Val Glu Glu Ala Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu
 145 150 155 160
 Ala Asn Tyr Glu Ile Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile
 165 170 175
 Thr Arg Pro Leu His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val
 180 185 190
 Ala Lys Lys Leu Ala Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val
 195 200 205
 Ile Gly Tyr Ile Val Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala
 210 215 220

Ile Leu Ala Glu Glu Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu
 225 230 235 240

Tyr Tyr Ile Glu Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu
 245 250 255

Gly Phe Gly Tyr Arg Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln
 260 265 270

Val Gly Leu Thr Ser Trp Leu Asn Ile Lys Lys
 275 280

<210> 3
 <211> 493
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: BlastP
 alignment Pyrococcus sp. GB-D DNA polymerase (Deep
 Vent) subject sequence

<400> 3
 Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile
 1 5 10 15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
 20 25 30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Gln Ile
 35 40 45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
 50 55 60

Ile Ile Asp Ala Glu Lys Val Arg Lys Lys Phe Leu Gly Arg Pro Ile
 65 70 75 80

Glu Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
 85 90 95

Arg Asp Lys Ile Arg Glu His Ser Ala Val Ile Asp Ile Phe Glu Tyr
 100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125

Met Glu Gly Asp Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
 130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
 145 150 155 160

Ser Tyr Ala Asp Glu Glu Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
 165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
 180 185 190

Arg Phe Leu Lys Val Ile Arg Glu Lys Asp Pro Asp Val Ile Ile Thr
 195 200 205
 Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Val Lys Arg Ala Glu
 210 215 220
 Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
 225 230 235 240
 Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile
 245 250 255
 His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
 260 265 270
 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
 275 280 285
 Lys Val Tyr Ala His Glu Ile Ala Glu Ala Trp Glu Thr Gly Lys Gly
 290 295 300
 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr
 305 310 315 320
 Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
 325 330 335
 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
 340 345 350
 Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
 355 360 365
 Pro Asn Lys Pro Asp Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
 370 375 380
 Tyr Ala Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Gly
 385 390 395 400
 Leu Val Ser Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
 405 410 415
 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Glu Tyr
 420 425 430
 Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
 435 440 445
 Phe Ile Pro Ser Leu Leu Lys Arg Leu Leu Asp Glu Arg Gln Glu Ile
 450 455 460
 Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Lys Met Leu
 465 470 475 480
 Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser
 485 490

<210> 4
 <211> 283
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:BlastP
 alignment Pyrococcus sp. GB-D DNA polymerase (Deep
 Vent) subject sequence

<400> 4

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Asn Ser Tyr Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys
 1           5           10           15

Lys Glu Cys Ala Glu Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu
          20           25           30

Phe Val Arg Lys Glu Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr
          35           40           45

Ile Asp Thr Asp Gly Leu Tyr Ala Thr Ile Pro Gly Ala Lys Pro Glu
          50           55           60

Glu Ile Lys Lys Lys Ala Leu Glu Phe Val Asp Tyr Ile Asn Ala Lys
          65           70           75           80

Leu Pro Gly Leu Leu Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly
          85           90           95

Phe Phe Val Thr Lys Lys Lys Tyr Ala Leu Ile Asp Glu Glu Gly Lys
          100          105          110

Ile Ile Thr Arg Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile
          115          120          125

Ala Lys Glu Thr Gln Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly
          130          135          140

Asn Val Glu Glu Ala Val Lys Ile Val Lys Glu Val Thr Glu Lys Leu
          145          150          155          160

Ser Lys Tyr Glu Ile Pro Pro Glu Lys Leu Val Ile Tyr Glu Gln Ile
          165          170          175

Thr Arg Pro Leu His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val
          180          185          190

Ala Lys Arg Leu Ala Ala Arg Gly Val Lys Val Arg Pro Gly Met Val
          195          200          205

Ile Gly Tyr Ile Val Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala
          210          215          220

Ile Leu Ala Glu Glu Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu
          225          230          235          240

Tyr Tyr Ile Glu Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu
          245          250          255

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Ala Phe Gly Tyr Arg Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln
260 265 270

Thr Gly Leu Thr Ala Trp Leu Asn Ile Lys Lys
275 280

<210> 5
<211> 493
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:BlastP
alignment consensus sequence

<220>
<221> MOD_RES
<222> (1)..(493)
<223> Xaa = unknown amino acid

<400> 5
Met Ile Leu Asp Xaa Asp Tyr Ile Thr Glu Xaa Gly Lys Pro Xaa Ile
1 5 10 15
Arg Xaa Phe Lys Lys Glu Asn Gly Xaa Phe Lys Xaa Glu Xaa Asp Arg
20 25 30
Xaa Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Xaa Asp Asp Ser Xaa Ile
35 40 45
Xaa Glu Val Xaa Lys Ile Thr Xaa Glu Arg His Gly Lys Ile Val Arg
50 55 60
Ile Xaa Asp Xaa Glu Lys Val Xaa Lys Lys Phe Leu Gly Xaa Pro Ile
65 70 75 80
Xaa Val Trp Xaa Leu Tyr Xaa Glu His Pro Gln Asp Val Pro Xaa Ile
85 90 95
Arg Xaa Lys Xaa Arg Glu His Xaa Ala Val Xaa Asp Ile Phe Glu Tyr
100 105 110
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115 120 125
Met Glu Gly Xaa Glu Glu Leu Lys Xaa Leu Ala Phe Asp Ile Glu Thr
130 135 140
Leu Tyr His Glu Gly Glu Glu Phe Xaa Lys Gly Pro Ile Ile Met Ile
145 150 155 160
Ser Tyr Ala Asp Glu Xaa Glu Ala Lys Val Ile Thr Trp Lys Xaa Ile
165 170 175
Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
180 185 190
Arg Phe Leu Xaa Xaa Ile Arg Glu Lys Asp Pro Asp Xaa Ile Xaa Thr
195 200 205

Tyr	Asn	Gly	Asp	Ser	Phe	Asp	Xaa	Pro	Tyr	Leu	Xaa	Lys	Arg	Ala	Glu	210	215	220
Lys	Leu	Gly	Ile	Lys	Leu	Xaa	Xaa	Gly	Arg	Asp	Gly	Ser	Glu	Pro	Lys	225	230	235
Met	Gln	Arg	Xaa	Gly	Asp	Met	Thr	Ala	Val	Glu	Xaa	Lys	Gly	Arg	Ile	245	250	255
His	Phe	Asp	Leu	Tyr	His	Val	Ile	Xaa	Arg	Thr	Ile	Asn	Leu	Pro	Thr	260	265	270
Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Ile	Phe	Gly	Lys	Pro	Lys	Glu	275	280	285
Lys	Val	Tyr	Ala	Xaa	Glu	Ile	Ala	Xaa	Ala	Trp	Glu	Xaa	Gly	Xaa	Xaa	290	295	300
Leu	Glu	Arg	Val	Ala	Lys	Tyr	Ser	Met	Glu	Asp	Ala	Lys	Xaa	Thr	Tyr	305	310	315
Glu	Leu	Gly	Xaa	Glu	Phe	Xaa	Pro	Met	Glu	Xaa	Gln	Leu	Ser	Arg	Leu	325	330	335
Val	Gly	Gln	Pro	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu	340	345	350
Val	Glu	Trp	Xaa	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Xaa	Ala	355	360	365
Pro	Asn	Lys	Pro	Xaa	Glu	Xaa	Glu	Tyr	Xaa	Arg	Arg	Leu	Arg	Glu	Ser	370	375	380
Tyr	Xaa	Gly	Gly	Xaa	Val	Lys	Glu	Pro	Glu	Lys	Gly	Leu	Trp	Glu	Xaa	385	390	395
Xaa	Val	Xaa	Leu	Asp	Phe	Arg	Xaa	Leu	Tyr	Pro	Ser	Ile	Ile	Ile	Thr	405	410	415
His	Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Xaa	Glu	Gly	Cys	Xaa	Xaa	Tyr	420	425	430
Asp	Xaa	Ala	Pro	Xaa	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Xaa	Pro	Gly	435	440	445
Phe	Ile	Pro	Ser	Leu	Leu	Xaa	Xaa	Leu	Leu	Xaa	Glu	Arg	Gln	Xaa	Ile	450	455	460
Lys	Xaa	Lys	Met	Lys	Xaa	Xaa	Xaa	Asp	Pro	Ile	Glu	Lys	Xaa	Xaa	Leu	465	470	475
Asp	Tyr	Arg	Gln	Xaa	Ala	Ile	Lys	Xaa	Leu	Ala	Asn	Ser				485	490	

<210> 6

<211> 283

<212> PRT

<213> Artificial Sequence


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<220>
<223> Description of Artificial Sequence:BlastP
      alignment consensus sequence

<220>
<221> MOD_RES
<222> (1)..(283)
<223> Xaa = unknown amino acid

<400> 6
Asn Ser Xaa Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys
 1             5             10             15

Lys Glu Cys Ala Glu Ser Val Thr Ala Trp Gly Arg Xaa Tyr Ile Glu
          20             25             30

Xaa Val Xaa Lys Glu Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr
          35             40             45

Ile Asp Thr Asp Gly Leu Tyr Ala Thr Ile Pro Gly Xaa Xaa Xaa Glu
          50             55             60

Glu Ile Lys Lys Lys Ala Leu Glu Phe Val Xaa Tyr Ile Asn Xaa Lys
          65             70             75             80

Leu Pro Gly Leu Leu Glu Leu Glu Tyr Glu Gly Phe Tyr Xaa Arg Gly
          85             90             95

Phe Phe Val Thr Lys Lys Xaa Tyr Ala Xaa Ile Asp Glu Glu Gly Lys
          100            105            110

Xaa Ile Thr Arg Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile
          115            120            125

Ala Lys Glu Thr Gln Ala Xaa Val Leu Glu Xaa Ile Leu Lys His Gly
          130            135            140            145

Xaa Val Glu Glu Ala Val Xaa Ile Val Lys Glu Val Xaa Xaa Lys Leu
          145            150            155            160

Xaa Xaa Tyr Glu Ile Pro Pro Glu Lys Leu Xaa Ile Tyr Glu Gln Ile
          165            170            175

Thr Arg Pro Leu His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val
          180            185            190

Ala Lys Xaa Leu Ala Ala Xaa Gly Val Lys Xaa Xaa Pro Gly Met Val
          195            200            205

Ile Gly Tyr Ile Val Leu Arg Gly Asp Gly Pro Ile Ser Xaa Arg Ala
          210            215            220

Ile Leu Ala Glu Glu Xaa Asp Xaa Xaa Lys His Lys Tyr Asp Ala Glu
          225            230            235            240

Tyr Tyr Ile Glu Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu
          245            250            255

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Xaa Phe Gly Tyr Arg Lys Glu Asp Leu Arg Xaa Gln Lys Thr Xaa Gln
260 265 270

Xaa Gly Leu Thr Xaa Trp Leu Asn Ile Lys Lys
275 280

<210> 7
<211> 151
<212> PRT
<213> Escherichia coli

<220>
<223> mesophile E. coli deoxyuridine 5'-triphosphate
nucleotidohydrolase (dUTPase or Dut) (ECD)

<400> 7
Met Lys Lys Ile Asp Val Lys Ile Leu Asp Pro Arg Val Gly Lys Glu
1 5 10 15
Phe Pro Leu Pro Thr Tyr Ala Thr Ser Gly Ser Ala Gly Leu Asp Leu
20 25 30
Arg Ala Cys Leu Asn Asp Ala Val Glu Leu Ala Pro Gly Asp Thr Thr
35 40 45
Leu Val Pro Thr Gly Leu Ala Ile His Ile Ala Asp Pro Ser Leu Ala
50 55 60
Ala Met Met Leu Pro Arg Ser Gly Leu Gly His Lys His Gly Ile Val
65 70 75 80
Leu Gly Asn Leu Val Gly Leu Ile Asp Ser Asp Tyr Gln Gly Gln Leu
85 90 95
Met Ile Ser Val Trp Asn Arg Gly Gln Asp Ser Phe Thr Ile Gln Pro
100 105 110
Gly Glu Arg Ile Ala Gln Met Ile Phe Val Pro Val Val Gln Ala Glu
115 120 125
Phe Asn Leu Val Glu Asp Phe Asp Ala Thr Asp Arg Gly Glu Gly Gly
130 135 140
Phe Gly His Ser Gly Arg Gln
145 150

<210> 8
<211> 150
<212> PRT
<213> Aquifex aeolicus

<220>
<223> deoxyuridine 5'-triphosphate nucleotidohydrolase
(dUTPase or Dut) (AAD)

<400> 8
Met Ser Lys Val Ile Leu Lys Ile Lys Arg Leu Pro His Ala Gln Asp
1 5 10 15

Leu Pro Leu Pro Ser Tyr Ala Thr Pro His Ser Ser Gly Leu Asp Leu
 20 25 30
 Arg Ala Ala Ile Glu Lys Pro Leu Lys Ile Lys Pro Phe Glu Arg Val
 35 40 45
 Leu Ile Pro Thr Gly Leu Ile Leu Glu Ile Pro Glu Gly Tyr Glu Gly
 50 55 60
 Gln Val Arg Pro Arg Ser Gly Leu Ala Trp Lys Lys Gly Leu Thr Val
 65 70 75 80
 Leu Asn Ala Pro Gly Thr Ile Asp Ala Asp Tyr Arg Gly Glu Val Lys
 85 90 95
 Val Ile Leu Val Asn Leu Gly Asn Glu Glu Val Val Ile Glu Arg Gly
 100 105 110
 Glu Arg Ile Ala Gln Leu Val Ile Ala Pro Val Gln Arg Val Glu Val
 115 120 125
 Val Glu Val Glu Glu Val Ser Gln Thr Gln Arg Gly Glu Gly Gly Phe
 130 135 140
 Gly Ser Thr Gly Thr Lys
 145 150

<210> 9
 <211> 149
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:E. coli
 deoxyuridine 5'-triphosphate nucleotidohydrolase
 (dUTPase or Dut) (ECD) BlastP alignment sequence

<400> 9
 Met Lys Lys Ile Asp Val Lys Ile Leu Asp Pro Arg Val Gly Lys Glu
 1 5 10 15
 Phe Pro Leu Pro Thr Tyr Ala Thr Ser Gly Ser Ala Gly Leu Asp Leu
 20 25 30
 Arg Ala Cys Leu Asn Asp Ala Val Glu Leu Ala Pro Gly Asp Thr Thr
 35 40 45
 Leu Val Pro Thr Gly Leu Ala Ile His Ile Ala Asp Pro Ser Leu Ala
 50 55 60
 Ala Met Met Leu Pro Arg Ser Gly Leu Gly His Lys His Gly Ile Val
 65 70 75 80
 Leu Gly Asn Leu Val Gly Leu Ile Asp Ser Asp Tyr Gln Gly Gln Leu
 85 90 95
 Met Ile Ser Val Trp Asn Arg Gly Gln Asp Ser Phe Thr Ile Gln Pro
 100 105 110

Gly Glu Arg Ile Ala Gln Met Ile Phe Val Pro Val Val Gln Ala Glu
115 120 125

Phe Asn Leu Val Glu Asp Phe Asp Ala Thr Asp Arg Gly Glu Gly Gly
130 135 140

Phe Gly His Ser Gly
145

<210> 10
<211> 148
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Aquifex
aeolicus deoxyuridine 5'-triphosphate
nucleotidohydrolase (dUTPase or Dut) (AAD) BlastP
alignment sequence

<400> 10
Met Ser Lys Val Ile Leu Lys Ile Lys Arg Leu Pro His Ala Gln Asp
1 5 10 15

Leu Pro Leu Pro Ser Tyr Ala Thr Pro His Ser Ser Gly Leu Asp Leu
20 25 30

Arg Ala Ala Ile Glu Lys Pro Leu Lys Ile Lys Pro Phe Glu Arg Val
35 40 45

Leu Ile Pro Thr Gly Leu Ile Leu Glu Ile Pro Glu Gly Tyr Glu Gly
50 55 60

Gln Val Arg Pro Arg Ser Gly Leu Ala Trp Lys Lys Gly Leu Thr Val
65 70 75 80

Leu Asn Ala Pro Gly Thr Ile Asp Ala Asp Tyr Arg Gly Glu Val Lys
85 90 95

Val Ile Leu Val Asn Leu Gly Asn Glu Glu Val Val Ile Glu Arg Gly
100 105 110

Glu Arg Ile Ala Gln Leu Val Ile Ala Pro Val Gln Arg Val Glu Val
115 120 125

Val Glu Val Glu Glu Val Ser Gln Thr Gln Arg Gly Glu Gly Gly Phe
130 135 140

Gly Ser Thr Gly
145

<210> 11
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
sequence

<400> 11
Gly Leu Asp Leu Arg Ala
1 5

<210> 12
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
sequence

<400> 12
Pro Thr Gly Leu
1

<210> 13
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
sequence

<400> 13
Pro Arg Ser Gly Leu
1 5

<210> 14
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
sequence

<400> 14
Gly Glu Arg Ile Ala Gln
1 5

<210> 15
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
sequence

<400> 15
Arg Gly Glu Gly Gly Phe Gly
1 5

<210> 16
 <211> 459
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus
 sequence, minimal encoding sequence using
 preferred E. coli codons

<400> 16
 atgarmaaar ttrwtstgaa aattmwgsrt cygcstswtg scmaagawtt wccgctgccg 60
 asctatgcga ccyctsrcag ckcaggcctg gatctgcgtg cgkscmttra saawscgstg 120
 raamttrmgc cgkktgawas grygctgrtt cgcaccggcc tgrycmttsa wattscggaw 180
 ssttmtctgg mggsgmwgrt gckgccgcgt agcggcctgg scyrkaaama kggcwtaryg 240
 stgskgaacs ygsygggcmg gattgatrsc gattatcrgg gcsaastgaw grttakcstg 300
 kkgaacckgg gcmasgawkm akttrygatt sagcsgggcg aacgtattgc gcagmtgrtt 360
 wttgygccgg tgswgcrppy ggaakttrwt swggtggaag awkttkmtsm gaccsakcgt 420
 ggcgaaggcg gctttggcym tascggcasa magtaatga 459

<210> 17
 <211> 151
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus
 sequence, minimal encoding sequence translation

<220>
 <221> MOD_RES
 <222> (2)
 <223> Xaa = Lys, Ser, Arg or Asn

<220>
 <221> MOD_RES
 <222> (4)
 <223> Xaa = Ile or Val

<220>
 <221> MOD_RES
 <222> (5)
 <223> Xaa = Asp, Ile, Val or Asn

<220>
 <221> MOD_RES
 <222> (6)
 <223> Xaa = Val or Leu

<220>
 <221> MOD_RES
 <222> (9)
 <223> Xaa = Leu, Lys, Gln or Met

<220>
 <221> MOD_RES
 <222> (10)
 <223> Xaa = Asp, Arg, Gly or His

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<220>
<221> MOD_RES
<222> (11)
<223> Xaa = Pro or Leu

<220>
<221> MOD_RES
<222> (12)
<223> Xaa = Arg or Pro

<220>
<221> MOD_RES
<222> (13)
<223> Xaa = Val, His, Asp or Leu

<220>
<221> MOD_RES
<222> (14)
<223> Xaa = Gly or Ala

<220>
<221> MOD_RES
<222> (15)
<223> Xaa = Lys or Gln

<220>
<221> MOD_RES
<222> (16)
<223> Xaa = Glu or Asp

<220>
<221> MOD_RES
<222> (17)
<223> Xaa = Phe or Leu

<220>
<221> MOD_RES
<222> (21)
<223> Xaa = Thr or Ser

<220>
<221> MOD_RES
<222> (25)
<223> Xaa = Ser or Pro

<220>
<221> MOD_RES
<222> (26)
<223> Xaa = Gly, His, Asp or Arg

<220>
<221> MOD_RES
<222> (28)
<223> Xaa = Ala or Ser

<220>
<221> MOD_RES
<222> (35)
<223> Xaa = Cys, Ala, Ser or Gly

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<220>
<221> MOD_RES
<222> (36)
<223> Xaa = Leu or Ile

<220>
<221> MOD_RES
<222> (37)
<223> Xaa = Asn, Glu, Lys or Asp

<220>
<221> MOD_RES
<222> (38)
<223> Xaa = Asp, Lys, Asn or Glu

<220>
<221> MOD_RES
<222> (39)
<223> Xaa = Ala or Pro

<220>
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<222> (40)
<223> Xaa = Val or Leu

<220>
<221> MOD_RES
<222> (41)
<223> Xaa = Glu or Lys

<220>
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<222> (42)
<223> Xaa = Leu or Ile

<220>
<221> MOD_RES
<222> (43)
<223> Xaa = Ala, Lys, Glu or Thr

<220>
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 20 25 30
 Arg Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa
 35 40 45
 Leu Xaa Pro Thr Gly Leu Xaa Xaa Xaa Ile Xaa Xaa Xaa Xaa Leu Xaa
 50 55 60
 Xaa Xaa Xaa Xaa Pro Arg Ser Gly Leu Xaa Xaa Lys Xaa Gly Xaa Xaa
 65 70 75 80

Xaa Xaa Asn Xaa Xaa Gly Xaa Ile Asp Xaa Asp Tyr Xaa Gly Glx Xaa
 85 90 95
 Xaa Xaa Xaa Xaa Xaa Asn Xaa Gly Xaa Xaa Xaa Xaa Xaa Ile Glx Xaa
 100 105 110
 Gly Glu Arg Ile Ala Gln Xaa Xaa Xaa Xaa Pro Val Xaa Xaa Xaa Glu
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 Xaa Xaa Xaa Val Glu Xaa Xaa Xaa Xaa Thr Xaa Arg Gly Glu Gly Gly
 130 135 140
 Phe Gly Xaa Xaa Gly Xaa Xaa
 145 150

<210> 18
 <211> 456
 <212> DNA
 <213> Artificial Sequence

<220>
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 sequence, minimal encoding sequence after removal
 of non-similar degeneracies and selection of AAD
 parent residues

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 raamttrmgc cgkktgawas grygctgrtt ccgaccggcc tgatcmttsa wattscggaw 180
 gggtmtgmgg sgcagrtgck gccgcgtagc ggcctggsct ggaaamakgg cwtarygstg 240
 ctgaacgcgs ygggcmygat tgaatrscgat tatcrgggcs aastgawgrt takcstgggtg 300
 aacckggggcm asgawgaakt trygattsag csgggcggaac gtattgcgca gmtgrttwtt 360
 gygccggtgs wgcrggygga akttrwtswg gtggaagawk tttctcagac csakcgtggc 420
 gaaggcggct ttggctctas cggcasamag taatga 456

<210> 19
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 <212> PRT
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<220>
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Xaa Pro Leu Pro Xaa Tyr Ala Thr Xaa His Ser Xaa Gly Leu Asp Leu
      20               25               30

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Arg Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa
 35 40 45
 Leu Xaa Pro Thr Gly Leu Ile Xaa Xaa Ile Xaa Xaa Gly Xaa Xaa Xaa
 50 55 60
 Gln Xaa Xaa Pro Arg Ser Gly Leu Xaa Trp Lys Xaa Gly Xaa Xaa Xaa
 65 70 75 80
 Leu Asn Ala Xaa Gly Xaa Ile Asp Xaa Asp Tyr Xaa Gly Glx Xaa Xaa
 85 90 95
 Xaa Xaa Xaa Asn Asn Xaa Gly Xaa Xaa Glu Xaa Xaa Ile Glx Xaa Gly
 100 105 110
 Glu Arg Ile Ala Gln Xaa Xaa Xaa Xaa Pro Val Xaa Xaa Xaa Glu Xaa
 115 120 125
 Xaa Xaa Val Glu Xaa Xaa Ser Gln Thr Xaa Arg Gly Glu Gly Gly Phe
 130 135 140
 Gly Ser Xaa Gly Xaa Xaa
 145 150

<210> 20
 <211> 487
 <212> DNA
 <213> Artificial Sequence

<220>
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 sequence, minimal encoding sequence after removal
 of non-similar degeneracies, selection of AAD parent
 residues, priming and restriction sites added to ends
 and codon usage changed to add restriction sites

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 scmttrasra wscgstgraa mtrrmgccgk ktgawasgry gctgrttccg accggtctga 180
 tcmttsawat tscggawggt tmtgmggsgc agrtgckgcc gcgtagcggc ctggsctgga 240
 aamakggcwt arygstgctg aacgcgsygg gcmygatcga trscgattat crgggcsaas 300
 tgawgrttak cstggtgaac ckgggcmasg awgaakttry gattsagcsg ggccaacgta 360
 ttgctgcagmt grttwttyg ccggtgswgc rgyyggaaakt trwtswggtg gaagawkttt 420
 ctcagaccsa kcggtggcgaa ggcggtctttg gctctascgg casamagtaa tgaggatccg 480
 aattctt 487

<210> 21
 <211> 150
 <212> PRT
 <213> Artificial Sequence

<220>
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<220>
<221> MOD_RES
<222> (120)
<223> Xaa = Phe or Ile

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<223> Xaa = Val or Ala

<220>
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<222> (124)
<223> Xaa = Val, Gln, Glu or Leu

<220>
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<223> Xaa = Gln or Arg

<220>
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<223> Xaa = Ala or Val

<220>
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<223> Xaa = Phe or Val

<220>
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<223> Xaa = Asn, Val, Ile or Asp

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<223> Xaa = Leu, Glu, Gln or Val

<220>
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<222> (133)
<223> Xaa = Asp or Glu

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<223> Xaa = Asp, Gln, Glu or His

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<222> (147)
<223> Xaa = Ser or Thr

<220>
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<222> (149)
<223> Xaa = Arg or Thr

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<220>
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 <223> Xaa = Gln or Lys

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 20 25 30

 Arg Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa
 35 40 45

 Leu Xaa Pro Thr Gly Leu Ile Xaa Xaa Ile Xaa Xaa Gly Xaa Xaa Xaa
 50 55 60

 Gln Xaa Xaa Pro Arg Ser Gly Leu Xaa Trp Lys Xaa Gly Xaa Xaa Xaa
 65 70 75 80

 Leu Asn Ala Xaa Gly Xaa Ile Asp Xaa Asp Tyr Xaa Gly Glx Xaa Xaa
 85 90 95

 Xaa Xaa Xaa Asn Asn Xaa Gly Xaa Xaa Glu Xaa Xaa Ile Glx Xaa Gly
 100 105 110

 Glu Arg Ile Ala Gln Xaa Xaa Xaa Xaa Pro Val Xaa Xaa Xaa Glu Xaa
 115 120 125

 Xaa Xaa Val Glu Xaa Xaa Ser Gln Thr Xaa Arg Gly Glu Gly Gly Phe
 130 135 140

 Gly Ser Xaa Gly Xaa Xaa
 145 150

<210> 22
 <211> 2349
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Pfu/Deep Vent
 hybrid DNA polymerase minimal encoding sequence

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 ctgctgarag atgattctma gattgakgaa gttaraaaaa tcaactgstga gcgccatggc 180
 aagattgttc gtatcrttga tgyggaaaag gtarrgaaga aatttctggg caraccaatc 240
 rmgggtgtgga ractgtatyt cgaacatcca caagatgttc cgaytattcg cgakaaartt 300
 cgcgaaacaty ctgcagttrt tgacatcttc gaatacgata ttccatttgc aaagcggttac 360
 ctcatcgaca aaggcctgat accaatggag ggcgakgaag aactcaagmt cctggcggtc 420
 gatatagaaa cctctatca cgaaggcgaa gagtttgsta aaggcccaat tataatgatt 480
 agctatgcag atgaaramga agcaaagggtg attacttgga aaaamataga tctcccatac 540
 gttgagggtt tatcttccga gcgcgagatg attaacgcgt ttctcarart tatccgcgag 600
 aaggatccgg acrttatcrt tacttataac ggcgactctt ttgacytccc atatctggyg 660
 aaacgcgcag aaaaactcgg tattaaactg mctmtcggcc gtgatgggtc cgagccgaag 720
 atgcagcgtm tcggcgatat gaccgctgta gaarttaagg gtcgtatcca tttcgacctg 780
 tatcatgtaa ttmsccgtac tattaacctc ccgacttaca ctctcgaggc tgtatatgaa 840

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gcaatttttg gtaagccgaa ggagaaggta tacgccsatg agattgcara ggcgtgggaa 900
wccggtragr rcctcgagcg tgttgcaaaa tactccatgg aagatgcaaa ggygacttat 960
gaactcggca ragaattcyt cccaatggaa rycagctct ctcgcctggg tggccaacca 1020
ctgtgggatg tttctcgttc ttccaccggg aacctcgtag agtgggtwtct cctgcgcaaa 1080
gcgtacgaac gcaacgaast ggctccgaac aagccakmcg aasragagta tsaacgccgt 1140
ctccgcgagt cttacrcctgg tggctwtggt aaagagccag aaaagggcct ctgggaarrc 1200
mtcgtgtmcc tcgatttttcg ckctctgtat ccgctctatta tcattacca caacgtgtct 1260
ccggatactc tcaacckcga gggctgcara ramtatgatr ttgctccgsa agtaggccac 1320
aagtctctga aggacwtccc gggcttttatt ccgctctctcc tgrrgcrctc gctcgakgaa 1380
cgccaaraga ttaagmscaa aatgaaggmg wccmaggatc cgattgaaaa aawamtgctc 1440
gactatcgcc aaaragcgat taaamtccct gcaaactctt wttacggcta ttatggctat 1500
gcaaaagcac gctggctactg taaggagtgt gctgagtcgg ttactgcttg gggtcgcraa 1560
tacatcgagy tcgtgyggaa ggagctcgaa gaaaagtttg gctttaaagt tctctacatt 1620
gacactgatg gtctctatgc gactattccg ggtgstragy ctgaggaaat taagaaaaag 1680
gctctcgaat ttgtgaaata cattaackcg aagctcccgg gtctcctgga gctcgaatat 1740
gaaggctttt atrwgcgcgg cttcttcggt accaagaaga ratatgcgst gattgatgaa 1800
gaaggcaaar ttattactcg tggctcogag attgtgcgcc gtgattggag cgaaattgag 1860
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gtgaraattg taaaagaagt aaycsaaaag ctckctaamt atgaaattcc gccagagaag 1980
ctcgygattt atgagcagat tactcgcccc ctgcatgagt ataaggcgat tggctccgcac 2040
gtggctgttg caaagaract ggctgctara ggcgtgaaar ttaraccggg tatggtaatt 2100
ggctacattg tactccgcgg cgatggctcg attagcaamc gtgcaattct agctgaggaa 2160
twcgatcyga raaagcacia gtatgacgca gaatattaca ttgagaacca ggtgctcccg 2220
gcggtactcc gtattctgga ggsttttggc taccgtaagg aagacctccg ctrscaaaag 2280
actaracagr ytggcctcac tkcttggtc aacattaaaa aatccggtac ccactagtgc 2340
tagcatgac 2349

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<210> 23
<211> 778
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:Pfu/Deep Vent
      hybrid DNA polymerase minimal encoding sequence
      translation

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<223> Xaa = Val or Ile

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<223> Xaa = Leu or Ile

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<223> Xaa = Arg or Lys

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 20 25 30
 Xaa Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Xaa Asp Asp Ser Xaa Ile
 35 40 45
 Xaa Glu Val Xaa Lys Ile Thr Xaa Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Xaa Asp Xaa Glu Lys Val Xaa Lys Lys Phe Leu Gly Xaa Pro Ile
 65 70 75 80

Xaa	Val	Trp	Xaa	Leu	Tyr	Xaa	Glu	His	Pro	Gln	Asp	Val	Pro	Xaa	Ile	85	90	95
Arg	Xaa	Lys	Xaa	Arg	Glu	His	Xaa	Ala	Val	Xaa	Asp	Ile	Phe	Glu	Tyr	100	105	110
Asp	Ile	Pro	Phe	Ala	Lys	Arg	Tyr	Leu	Ile	Asp	Lys	Gly	Leu	Ile	Pro	115	120	125
Met	Glu	Gly	Xaa	Glu	Glu	Leu	Lys	Xaa	Leu	Ala	Phe	Asp	Ile	Glu	Thr	130	135	140
Leu	Tyr	His	Glu	Gly	Glu	Glu	Phe	Xaa	Lys	Gly	Pro	Ile	Ile	Met	Ile	145	150	155
Ser	Tyr	Ala	Asp	Glu	Xaa	Glu	Ala	Lys	Val	Ile	Thr	Trp	Lys	Xaa	Ile	165	170	175
Asp	Leu	Pro	Tyr	Val	Glu	Val	Val	Ser	Ser	Glu	Arg	Glu	Met	Ile	Lys	180	185	190
Arg	Phe	Leu	Xaa	Xaa	Ile	Arg	Glu	Lys	Asp	Pro	Asp	Xaa	Ile	Xaa	Thr	195	200	205
Tyr	Asn	Gly	Asp	Ser	Phe	Asp	Xaa	Pro	Tyr	Leu	Xaa	Lys	Arg	Ala	Glu	210	215	220
Lys	Leu	Gly	Ile	Lys	Leu	Xaa	Xaa	Gly	Arg	Asp	Gly	Ser	Glu	Pro	Lys	225	230	235
Met	Gln	Arg	Xaa	Gly	Asp	Met	Thr	Ala	Val	Glu	Xaa	Lys	Gly	Arg	Ile	245	250	255
His	Phe	Asp	Leu	Tyr	His	Val	Ile	Xaa	Arg	Thr	Ile	Asn	Leu	Pro	Thr	260	265	270
Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Ile	Phe	Gly	Lys	Pro	Lys	Glu	275	280	285
Lys	Val	Tyr	Ala	Xaa	Glu	Ile	Ala	Xaa	Ala	Trp	Glu	Xaa	Gly	Xaa	Xaa	290	295	300
Leu	Glu	Arg	Val	Ala	Lys	Tyr	Ser	Met	Glu	Asp	Ala	Lys	Xaa	Thr	Tyr	305	310	315
Glu	Leu	Gly	Xaa	Glu	Phe	Xaa	Pro	Met	Glu	Xaa	Gln	Leu	Ser	Arg	Leu	325	330	335
Val	Gly	Gln	Pro	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu	340	345	350
Val	Glu	Trp	Xaa	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Xaa	Ala	355	360	365
Pro	Asn	Lys	Pro	Xaa	Glu	Xaa	Glu	Tyr	Glx	Arg	Arg	Leu	Arg	Glu	Ser	370	375	380
Tyr	Xaa	Gly	Gly	Xaa	Val	Lys	Glu	Pro	Glu	Lys	Gly	Leu	Trp	Glu	Xaa	385	390	395

Xaa Val Xaa Leu Asp Phe Arg Xaa Leu Tyr Pro Ser Ile Ile Ile Thr
405 410 415
His Asn Val Ser Pro Asp Thr Leu Asn Xaa Glu Gly Cys Xaa Xaa Tyr
420 425 430
Asp Xaa Ala Pro Glx Val Gly His Lys Phe Cys Lys Asp Xaa Pro Gly
435 440 445
Phe Ile Pro Ser Leu Leu Xaa Xaa Leu Leu Xaa Glu Arg Gln Xaa Ile
450 455 460
Lys Xaa Lys Met Lys Xaa Xaa Xaa Asp Pro Ile Glu Lys Xaa Xaa Leu
465 470 475 480
Asp Tyr Arg Gln Xaa Ala Ile Lys Xaa Leu Ala Asn Ser Xaa Tyr Gly
485 490 495
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
500 505 510
Ser Val Thr Ala Trp Gly Arg Xaa Tyr Ile Glu Xaa Val Xaa Lys Glu
515 520 525
Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
530 535 540
Leu Tyr Ala Thr Ile Pro Gly Xaa Xaa Xaa Glu Glu Ile Lys Lys Lys
545 550 555 560
Ala Leu Glu Phe Val Lys Tyr Ile Asn Xaa Lys Leu Pro Gly Leu Leu
565 570 575
Glu Leu Glu Tyr Glu Gly Phe Tyr Xaa Arg Gly Phe Phe Val Thr Lys
580 585 590
Lys Xaa Tyr Ala Xaa Ile Asp Glu Glu Gly Lys Xaa Ile Thr Arg Gly
595 600 605
Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
610 615 620
Ala Xaa Val Leu Glu Xaa Ile Leu Lys His Gly Asx Val Glu Glu Ala
625 630 635 640
Val Xaa Ile Val Lys Glu Val Xaa Glx Lys Leu Xaa Xaa Tyr Glu Ile
645 650 655
Pro Pro Glu Lys Leu Xaa Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
660 665 670
Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Xaa Leu Ala
675 680 685
Ala Xaa Gly Val Lys Xaa Xaa Pro Gly Met Val Ile Gly Tyr Ile Val
690 695 700
Leu Arg Gly Asp Gly Pro Ile Ser Xaa Arg Ala Ile Leu Ala Glu Glu
705 710 715 720

Xaa Asp Xaa Xaa Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Xaa Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Xaa Gln Lys Thr Xaa Gln Xaa Gly Leu Thr Xaa
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 Trp Leu Asn Ile Lys Lys Ser Gly Thr His
 770 775

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 <212> PRT
 <213> Artificial Sequence

<220>
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 Pyrococcus furiosus family B DNA polymerase (Pfu)

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 20 25 30
 Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
 35 40 45
 Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
 65 70 75 80
 Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
 85 90 95
 Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
 100 105 110
 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125
 Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
 130 135 140
 Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
 145 150 155 160
 Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
 165 170 175
 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
 180 185 190
 Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
 195 200 205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
210 215 220
Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
225 230 235 240
Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
245 250 255
His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
260 265 270
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
275 280 285
Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn
290 295 300
Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305 310 315 320
Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
325 330 335
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340 345 350
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
355 360 365
Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser
370 375 380
Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385 390 395 400
Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
405 410 415
His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr
420 425 430
Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
435 440 445
Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
450 455 460
Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu
465 470 475 480
Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
485 490 495
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
500 505 510
Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu
515 520 525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
 530 535 540
 Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys Lys
 545 550 555 560
 Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
 565 570 575
 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
 580 585 590
 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly
 595 600 605
 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala
 625 630 635 640
 Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile
 645 650 655
 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
 675 680 685
 Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr Ser
 755 760 765
 Trp Leu Asn Ile Lys Lys Ser
 770 775

<210> 25

<211> 775

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:parent
 Pyrococcus sp. GD-B (Deep Vent) DNA polymerase

<400> 25

Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile
 1 5 10 15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
 20 25 30
 Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Gln Ile
 35 40 45
 Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Ile Asp Ala Glu Lys Val Arg Lys Lys Phe Leu Gly Arg Pro Ile
 65 70 75 80
 Glu Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
 85 90 95
 Arg Asp Lys Ile Arg Glu His Ser Ala Val Ile Asp Ile Phe Glu Tyr
 100 105 110
 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125
 Met Glu Gly Asp Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
 130 135 140
 Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
 145 150 155 160
 Ser Tyr Ala Asp Glu Glu Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
 165 170 175
 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
 180 185 190
 Arg Phe Leu Lys Val Ile Arg Glu Lys Asp Pro Asp Val Ile Ile Thr
 195 200 205
 Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Val Lys Arg Ala Glu
 210 215 220
 Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
 225 230 235 240
 Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile
 245 250 255
 His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
 260 265 270
 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
 275 280 285
 Lys Val Tyr Ala His Glu Ile Ala Glu Ala Trp Glu Thr Gly Lys Gly
 290 295 300
 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr
 305 310 315 320
 Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
 325 330 335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340 345 350
Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
355 360 365
Pro Asn Lys Pro Asp Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
370 375 380
Tyr Ala Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Gly
385 390 395 400
Leu Val Ser Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
405 410 415
His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Glu Tyr
420 425 430
Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
435 440 445
Phe Ile Pro Ser Leu Leu Lys Arg Leu Leu Asp Glu Arg Gln Glu Ile
450 455 460
Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Lys Met Leu
465 470 475 480
Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly
485 490 495
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
500 505 510
Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Arg Lys Glu
515 520 525
Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
530 535 540
Leu Tyr Ala Thr Ile Pro Gly Ala Lys Pro Glu Glu Ile Lys Lys Lys
545 550 555 560
Ala Leu Glu Phe Val Asp Tyr Ile Asn Ala Lys Leu Pro Gly Leu Leu
565 570 575
Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys
580 585 590
Lys Lys Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
595 600 605
Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
610 615 620
Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625 630 635 640
Val Lys Ile Val Lys Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Ile
645 650 655

Pro Pro Glu Lys Leu Val Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
 675 680 685
 Ala Arg Gly Val Lys Val Arg Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Thr Gly Leu Thr Ala
 755 760 765
 Trp Leu Asn Ile Lys Lys Lys
 770 775

<210> 26
 <211> 783
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:designed hybrid
 polymerase from Figure 11

<220>
 <221> MOD_RES
 <222> (1)..(783)
 <223> Xaa = unknown amino acid

<400> 26
 Met Ile Leu Asp Xaa Asp Tyr Ile Thr Glu Xaa Gly Lys Pro Xaa Ile
 1 5 10 15
 Arg Xaa Phe Lys Lys Glu Asn Gly Xaa Phe Lys Xaa Glu Xaa Asp Arg
 20 25 30
 Xaa Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Xaa Asp Asp Ser Xaa Ile
 35 40 45
 Xaa Glu Val Xaa Lys Ile Thr Xaa Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Xaa Asp Xaa Glu Lys Val Xaa Lys Lys Phe Leu Gly Xaa Pro Ile
 65 70 75 80
 Xaa Val Trp Xaa Leu Tyr Xaa Glu His Pro Gln Asp Val Pro Xaa Ile
 85 90 95
 Arg Xaa Lys Xaa Arg Glu His Xaa Ala Val Xaa Asp Ile Phe Glu Tyr
 100 105 110

Asp	Ile	Pro	Phe	Ala	Lys	Arg	Tyr	Leu	Ile	Asp	Lys	Gly	Leu	Ile	Pro	115	120	125
Met	Glu	Gly	Xaa	Glu	Glu	Leu	Lys	Xaa	Leu	Ala	Phe	Asp	Ile	Glu	Thr	130	135	140
Leu	Tyr	His	Glu	Gly	Glu	Glu	Phe	Xaa	Lys	Gly	Pro	Ile	Ile	Met	Ile	145	150	155
Ser	Tyr	Ala	Asp	Glu	Xaa	Glu	Ala	Lys	Val	Ile	Thr	Trp	Lys	Xaa	Ile	165	170	175
Asp	Leu	Pro	Tyr	Val	Glu	Val	Val	Ser	Ser	Glu	Arg	Glu	Met	Ile	Lys	180	185	190
Arg	Phe	Leu	Xaa	Xaa	Ile	Arg	Glu	Lys	Asp	Pro	Asp	Xaa	Ile	Xaa	Thr	195	200	205
Tyr	Asn	Gly	Asp	Ser	Phe	Asp	Xaa	Pro	Tyr	Leu	Xaa	Lys	Arg	Ala	Glu	210	215	220
Lys	Leu	Gly	Ile	Lys	Leu	Xaa	Xaa	Gly	Arg	Asp	Gly	Ser	Glu	Pro	Lys	225	230	235
Met	Gln	Arg	Xaa	Gly	Asp	Met	Thr	Ala	Val	Glu	Xaa	Lys	Gly	Arg	Ile	245	250	255
His	Phe	Asp	Leu	Tyr	His	Val	Ile	Xaa	Arg	Thr	Ile	Asn	Leu	Pro	Thr	260	265	270
Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Ile	Phe	Gly	Lys	Pro	Lys	Glu	275	280	285
Lys	Val	Tyr	Ala	Xaa	Glu	Ile	Ala	Xaa	Ala	Trp	Glu	Xaa	Gly	Xaa	Xaa	290	295	300
Leu	Glu	Arg	Val	Ala	Lys	Tyr	Ser	Met	Glu	Asp	Ala	Lys	Xaa	Thr	Tyr	305	310	315
Glu	Leu	Gly	Xaa	Glu	Phe	Xaa	Pro	Met	Glu	Xaa	Gln	Leu	Ser	Arg	Leu	325	330	335
Val	Gly	Gln	Pro	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu	340	345	350
Val	Glu	Trp	Xaa	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Xaa	Ala	355	360	365
Pro	Asn	Lys	Pro	Xaa	Glu	Xaa	Glu	Tyr	Xaa	Arg	Arg	Leu	Arg	Glu	Ser	370	375	380
Tyr	Xaa	Gly	Gly	Xaa	Val	Lys	Glu	Pro	Glu	Lys	Gly	Leu	Trp	Glu	Xaa	385	390	395
Xaa	Val	Xaa	Leu	Asp	Phe	Arg	Xaa	Leu	Tyr	Pro	Ser	Ile	Ile	Ile	Thr	405	410	415
His	Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Xaa	Glu	Gly	Cys	Xaa	Xaa	Tyr	420	425	430

Asp	Xaa	Ala	Pro	Xaa	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Xaa	Pro	Gly	
		435					440					445				
Phe	Ile	Pro	Ser	Leu	Leu	Xaa	Xaa	Leu	Leu	Xaa	Glu	Arg	Gln	Xaa	Ile	
	450					455					460					
Lys	Xaa	Lys	Met	Lys	Xaa	Xaa	Xaa	Asp	Pro	Ile	Glu	Lys	Xaa	Xaa	Leu	
465					470					475					480	
Asp	Tyr	Arg	Gln	Xaa	Ala	Ile	Lys	Xaa	Leu	Ala	Asn	Ser	Xaa	Tyr	Gly	
				485					490					495		
Tyr	Tyr	Gly	Tyr	Ala	Lys	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Cys	Ala	Glu	
			500					505					510			
Ser	Val	Thr	Ala	Trp	Gly	Arg	Xaa	Tyr	Ile	Glu	Xaa	Val	Xaa	Lys	Glu	
		515					520					525				
Leu	Glu	Glu	Lys	Phe	Gly	Phe	Lys	Val	Leu	Tyr	Ile	Asp	Thr	Asp	Gly	
	530					535						540				
Leu	Tyr	Ala	Thr	Ile	Pro	Gly	Xaa	Xaa	Xaa	Glu	Glu	Ile	Lys	Lys	Lys	
545					550					555					560	
Ala	Leu	Glu	Phe	Val	Lys	Tyr	Ile	Asn	Xaa	Lys	Leu	Pro	Gly	Leu	Leu	
				565					570					575		
Glu	Leu	Glu	Tyr	Glu	Gly	Phe	Tyr	Xaa	Arg	Gly	Phe	Phe	Val	Thr	Lys	
			580					585					590			
Lys	Xaa	Tyr	Ala	Xaa	Ile	Asp	Glu	Glu	Gly	Lys	Xaa	Ile	Thr	Arg	Gly	
		595					600					605				
Leu	Glu	Ile	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	Thr	Gln	
	610					615					620					
Ala	Xaa	Val	Leu	Glu	Xaa	Ile	Leu	Lys	His	Gly	Xaa	Val	Glu	Glu	Ala	
625					630					635					640	
Val	Xaa	Ile	Val	Lys	Glu	Val	Xaa	Xaa	Lys	Leu	Xaa	Xaa	Tyr	Glu	Ile	
				645					650					655		
Pro	Pro	Glu	Lys	Leu	Xaa	Ile	Tyr	Glu	Gln	Ile	Thr	Arg	Pro	Leu	His	
			660					665					670			
Glu	Tyr	Lys	Ala	Ile	Gly	Pro	His	Val	Ala	Val	Ala	Lys	Xaa	Leu	Ala	
		675					680					685				
Ala	Xaa	Gly	Val	Lys	Xaa	Xaa	Pro	Gly	Met	Val	Ile	Gly	Tyr	Ile	Val	
	690					695					700					
Leu	Arg	Gly	Asp	Gly	Pro	Ile	Ser	Xaa	Arg	Ala	Ile	Leu	Ala	Glu	Glu	
705					710					715					720	
Xaa	Asp	Xaa	Xaa	Lys	His	Lys	Tyr	Asp	Ala	Glu	Tyr	Tyr	Ile	Glu	Asn	
				725					730					735		
Gln	Val	Leu	Pro	Ala	Val	Leu	Arg	Ile	Leu	Glu	Xaa	Phe	Gly	Tyr	Arg	
			740					745					750			

Lys Glu Asp Leu Arg Xaa Gln Lys Thr Xaa Gln Xaa Gly Leu Thr Xaa
755 760 765

Trp Leu Asn Ile Lys Lys Ser Gly Thr His Asn Cys Asn His Asp
770 775 780

<210> 27
<211> 845
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
polymerase HyS1 from Figure 11

<220>
<221> MOD_RES
<222> (472)
<223> Xaa = unknown amino acid

<400> 27
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile
1 5 10 15
Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Glu Tyr Asp Arg
20 25 30
Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
35 40 45
Glu Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
50 55 60
Ile Val Asp Val Glu Lys Val Arg Lys Lys Phe Leu Gly Arg Pro Ile
65 70 75 80
Lys Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
85 90 95
Arg Asp Lys Val Arg Glu His Pro Ala Val Ile Asp Ile Phe Glu Tyr
100 105 110
Asp Ile Ala Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115 120 125
Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
130 135 140
Leu Tyr His Gly Ser Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145 150 155 160
Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
165 170 175
Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
180 185 190
Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
195 200 205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
210 215 220
Lys Leu Gly Ile Lys Leu Thr Leu Gly Arg Asp Gly Cys Glu Ala Lys
225 230 235 240
Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
245 250 255
His Phe Asp Leu Tyr Tyr Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
260 265 270
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
275 280 285
Lys Val Tyr Ala Asp Asp Ile Ala Glu Ala Trp Glu Thr Gly Lys Gly
290 295 300
Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305 310 315 320
Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ala Gln Leu Ser Arg Leu
325 330 335
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340 345 350
Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
355 360 365
Pro Asn Lys Pro Tyr Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
370 375 380
Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Ser
385 390 395 400
Leu Val Ser Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
405 410 415
His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
420 425 430
Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
435 440 445
Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
450 455 460
Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
465 470 475 480
Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
485 490 495
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
500 505 510
Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
515 520 525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
 530 535 540
 Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
 545 550 555 560
 Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
 565 570 575
 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
 580 585 590
 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
 595 600 605
 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
 625 630 635 640
 Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
 645 650 655
 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
 675 680 685
 Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Phe Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Ala Gly Leu Thr Ala
 755 760 765
 Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Ala Thr Val
 770 775 780
 Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
 785 790 795 800
 Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
 805 810 815
 Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
 820 825 830
 Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
 835 840 845

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<210> 28
<211> 758
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
        polymerase Hyb2 from Figure 11

<220>
<221> MOD_RES
<222> (472)
<223> Xaa = unknown amino acid

<400> 28
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
 1             5             10             15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
          20             25             30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile
          35             40             45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
          50             55             60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
          65             70             75             80

Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
          85             90             95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr
          100            105            110

Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro
          115            120            125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
          130            135            140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
          145            150            155            160

Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
          165            170            175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
          180            185            190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
          195            200            205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
          210            215            220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
          225            230            235            240

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Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
 245 250 255
 His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
 260 265 270
 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
 275 280 285
 Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp
 290 295 300
 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr
 305 310 315 320
 Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu
 325 330 335
 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
 340 345 350
 Val Glu Trp Leu Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
 355 360 365
 Pro Asn Lys Pro Ala Glu Gln Glu Tyr Glu Arg Arg Leu Arg Glu Ser
 370 375 380
 Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asp
 385 390 395 400
 Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
 405 410 415
 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
 420 425 430
 Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
 435 440 445
 Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
 450 455 460
 Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
 465 470 475 480
 Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
 485 490 495
 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
 500 505 510
 Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
 515 520 525
 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
 530 535 540
 Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
 545 550 555 560

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile
 35 40 45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
 50 55 60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
 65 70 75 80

Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
 85 90 95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr
 100 105 110

Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
 130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
 145 150 155 160

Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
 165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
 180 185 190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
 195 200 205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
 210 215 220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
 225 230 235 240

Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
 245 250 255

His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
 260 265 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
 275 280 285

Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp
 290 295 300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr
 305 310 315 320

Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu
 325 330 335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
 340 345 350

Val	Glu	Trp	Leu	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Leu	Ala	355	360	365	
Pro	Asn	Lys	Pro	Ala	Glu	Gln	Glu	Tyr	Glu	Arg	Arg	Leu	Arg	Glu	Ser	370	375	380	
Tyr	Thr	Gly	Gly	Phe	Val	Lys	Glu	Pro	Glu	Lys	Gly	Leu	Trp	Glu	Asp	385	390	395	400
Leu	Val	Ser	Leu	Asp	Phe	Arg	Ala	Leu	Tyr	Pro	Ser	Ile	Ile	Ile	Thr	405	410	415	
His	Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Arg	Glu	Gly	Cys	Lys	Asp	Tyr	420	425	430	
Asp	Ile	Ala	Pro	Glu	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Phe	Leu	Gly	435	440	445	
Phe	Ile	Pro	Ser	Leu	Leu	Gly	His	Leu	Leu	Glu	Glu	Arg	Gln	Glu	Ile	450	455	460	
Lys	Thr	Lys	Met	Lys	Glu	Thr	Xaa	Asp	Pro	Ile	Glu	Lys	Ile	Leu	Leu	465	470	475	480
Asp	Tyr	Arg	Gln	Lys	Ala	Ile	Lys	Leu	Leu	Ala	Asn	Ser	Tyr	Tyr	Gly	485	490	495	
Tyr	Tyr	Gly	Tyr	Ala	Lys	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Cys	Ala	Glu	500	505	510	
Ser	Val	Thr	Ala	Trp	Gly	Arg	Glu	Tyr	Ile	Glu	Phe	Val	Trp	Lys	Glu	515	520	525	
Leu	Glu	Glu	Lys	Phe	Gly	Phe	Lys	Val	Leu	Tyr	Ile	Asp	Thr	Asp	Gly	530	535	540	
Leu	Tyr	Ala	Thr	Ile	Pro	Gly	Gly	Glu	Pro	Glu	Glu	Ile	Lys	Lys	Lys	545	550	555	560
Ala	Leu	Glu	Phe	Val	Lys	Tyr	Ile	Asn	Ser	Lys	Leu	Pro	Gly	Leu	Leu	565	570	575	
Glu	Leu	Glu	Tyr	Glu	Gly	Phe	Tyr	Lys	Arg	Gly	Phe	Phe	Val	Thr	Lys	580	585	590	
Lys	Arg	Tyr	Ala	Val	Ile	Asp	Glu	Glu	Gly	Lys	Ile	Ile	Thr	Arg	Gly	595	600	605	
Leu	Glu	Ile	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	Thr	Gln	610	615	620	
Ala	Lys	Val	Leu	Glu	Ala	Ile	Leu	Lys	His	Gly	Asn	Val	Glu	Glu	Ala	625	630	635	640
Val	Lys	Ile	Val	Lys	Glu	Ile	Ile	Glu	Lys	Leu	Ala	Lys	Tyr	Glu	Ile	645	650	655	
Pro	Pro	Glu	Lys	Leu	Ala	Ile	Tyr	Glu	Gln	Ile	Thr	Arg	Pro	Leu	His	660	665	670	

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
 675 680 685
 Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Asn
 755

<210> 30
 <211> 845
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:hybrid
 polymerase HyS4 from Figure 11

<220>
 <221> MOD_RES
 <222> (472)
 <223> Xaa = unknown amino acid

<400> 30
 Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
 1 5 10 15
 Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
 20 25 30
 Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile
 35 40 45
 Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
 65 70 75 80
 Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
 85 90 95
 Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr
 100 105 110
 Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125
 Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
 130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
 145 150 155 160
 Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
 165 170 175
 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
 180 185 190
 Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
 195 200 205
 Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
 210 215 220
 Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
 225 230 235 240
 Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
 245 250 255
 His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
 260 265 270
 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
 275 280 285
 Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp
 290 295 300
 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr
 305 310 315 320
 Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu
 325 330 335
 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
 340 345 350
 Val Glu Trp Leu Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
 355 360 365
 Pro Asn Lys Pro Ala Glu Gln Glu Tyr Glu Arg Arg Leu Arg Glu Ser
 370 375 380
 Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asp
 385 390 395 400
 Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
 405 410 415
 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
 420 425 430
 Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
 435 440 445
 Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
 450 455 460

Lys	Thr	Lys	Met	Lys	Glu	Thr	Xaa	Asp	Pro	Ile	Glu	Lys	Ile	Leu	Leu	465	470	475	480
Asp	Tyr	Arg	Gln	Lys	Ala	Ile	Lys	Leu	Leu	Ala	Asn	Ser	Tyr	Tyr	Gly	485	490		495
Tyr	Tyr	Gly	Tyr	Ala	Lys	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Cys	Ala	Glu	500	505		510
Ser	Val	Thr	Ala	Trp	Gly	Arg	Glu	Tyr	Ile	Glu	Phe	Val	Trp	Lys	Glu	515	520		525
Leu	Glu	Glu	Lys	Phe	Gly	Phe	Lys	Val	Leu	Tyr	Ile	Asp	Thr	Asp	Gly	530	535		540
Leu	Tyr	Ala	Thr	Ile	Pro	Gly	Gly	Glu	Pro	Glu	Glu	Ile	Lys	Lys	Lys	545	550		555
Ala	Leu	Glu	Phe	Val	Lys	Tyr	Ile	Asn	Ser	Lys	Leu	Pro	Gly	Leu	Leu	565	570		575
Glu	Leu	Glu	Tyr	Glu	Gly	Phe	Tyr	Lys	Arg	Gly	Phe	Phe	Val	Thr	Lys	580	585		590
Lys	Arg	Tyr	Ala	Val	Ile	Asp	Glu	Glu	Gly	Lys	Ile	Ile	Thr	Arg	Gly	595	600		605
Leu	Glu	Ile	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	Thr	Gln	610	615		620
Ala	Lys	Val	Leu	Glu	Ala	Ile	Leu	Lys	His	Gly	Asn	Val	Glu	Glu	Ala	625	630		635
Val	Lys	Ile	Val	Lys	Glu	Ile	Ile	Glu	Lys	Leu	Ala	Lys	Tyr	Glu	Ile	645	650		655
Pro	Pro	Glu	Lys	Leu	Ala	Ile	Tyr	Glu	Gln	Ile	Thr	Arg	Pro	Leu	His	660	665		670
Glu	Tyr	Lys	Ala	Ile	Gly	Pro	His	Val	Ala	Val	Ala	Lys	Lys	Leu	Ala	675	680		685
Ala	Arg	Gly	Val	Lys	Ile	Lys	Pro	Gly	Met	Val	Ile	Gly	Tyr	Ile	Val	690	695		700
Leu	Arg	Gly	Asp	Gly	Pro	Ile	Ser	Lys	Arg	Ala	Ile	Leu	Ala	Glu	Glu	705	710		715
Phe	Asp	Pro	Lys	Lys	His	Lys	Tyr	Asp	Ala	Glu	Tyr	Tyr	Ile	Glu	Asn	725	730		735
Gln	Val	Leu	Pro	Ala	Val	Leu	Arg	Ile	Leu	Glu	Gly	Phe	Gly	Tyr	Arg	740	745		750
Lys	Glu	Asp	Leu	Arg	Trp	Gln	Lys	Thr	Lys	Gln	Ala	Gly	Leu	Thr	Ala	755	760		765
Trp	Leu	Asn	Ile	Lys	Lys	Ser	Gly	Thr	Gly	Gly	Gly	Gly	Ala	Thr	Val	770	775		780

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785 790 795 800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
805 810 815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
820 825 830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
835 840 845

<210> 31

<211> 845

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid
polymerase PhS1 from Figure 11

<400> 31

Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
1 5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Glu His Asp Arg
20 25 30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
35 40 45

Glu Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
50 55 60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65 70 75 80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
85 90 95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115 120 125

Met Glu Gly Asp Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145 150 155 160

Ser Tyr Ala Asp Glu Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
180 185 190

Arg Phe Leu Lys Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
195 200 205

Tyr	Asn	Gly	Asp	Ser	Phe	Asp	Leu	Pro	Tyr	Leu	Ala	Lys	Arg	Ala	Glu	210	215	220
Lys	Leu	Gly	Ile	Lys	Leu	Thr	Ile	Gly	Arg	Asp	Gly	Ser	Glu	Pro	Lys	225	230	235
Met	Gln	Arg	Ile	Gly	Asp	Met	Thr	Ala	Val	Glu	Val	Lys	Gly	Arg	Ile	245	250	255
His	Phe	Asp	Leu	Tyr	His	Val	Ile	Arg	Arg	Thr	Ile	Asn	Leu	Pro	Thr	260	265	270
Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Ile	Phe	Gly	Lys	Pro	Lys	Glu	275	280	285
Lys	Val	Tyr	Ala	Asp	Glu	Ile	Ala	Lys	Ala	Trp	Glu	Thr	Gly	Glu	Gly	290	295	300
Leu	Glu	Arg	Val	Ala	Lys	Tyr	Ser	Met	Glu	Asp	Ala	Lys	Ala	Thr	Tyr	305	310	315
Glu	Leu	Gly	Lys	Glu	Phe	Phe	Pro	Met	Glu	Ala	Gln	Leu	Ser	Arg	Leu	325	330	335
Val	Gly	Gln	Pro	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu	340	345	350
Val	Glu	Trp	Phe	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Leu	Ala	355	360	365
Pro	Asn	Lys	Pro	Asp	Glu	Arg	Glu	Tyr	Glu	Arg	Arg	Leu	Arg	Glu	Ser	370	375	380
Tyr	Ala	Gly	Gly	Phe	Val	Lys	Glu	Pro	Glu	Lys	Gly	Leu	Trp	Glu	Asn	385	390	395
Ile	Val	Ser	Leu	Asp	Phe	Arg	Ala	Leu	Tyr	Pro	Ser	Ile	Ile	Ile	Thr	405	410	415
His	Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Arg	Glu	Gly	Cys	Arg	Asn	Tyr	420	425	430
Asp	Val	Ala	Pro	Glu	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Phe	Pro	Gly	435	440	445
Phe	Ile	Pro	Ser	Leu	Leu	Lys	Arg	Leu	Leu	Asp	Glu	Arg	Gln	Lys	Ile	450	455	460
Lys	Thr	Lys	Met	Lys	Ala	Ser	Gln	Asp	Pro	Ile	Glu	Lys	Ile	Met	Leu	465	470	475
Asp	Tyr	Arg	Gln	Arg	Ala	Ile	Lys	Ile	Leu	Ala	Asn	Ser	Tyr	Tyr	Gly	485	490	495
Tyr	Tyr	Gly	Tyr	Ala	Lys	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Cys	Ala	Glu	500	505	510
Ser	Val	Thr	Ala	Trp	Gly	Arg	Glu	Tyr	Ile	Glu	Phe	Val	Trp	Lys	Glu	515	520	525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
 530 535 540
 Leu Tyr Ala Thr Ile Pro Gly Gly Lys Ser Glu Glu Ile Lys Lys Lys
 545 550 555 560
 Ala Leu Glu Phe Val Asp Tyr Ile Asn Ala Lys Leu Pro Gly Leu Leu
 565 570 575
 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
 580 585 590
 Lys Lys Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
 595 600 605
 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Arg Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
 625 630 635 640
 Val Arg Ile Val Lys Glu Val Thr Gln Lys Leu Ser Lys Tyr Glu Ile
 645 650 655
 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
 675 680 685
 Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Tyr Asp Pro Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Thr Gly Leu Thr Ser
 755 760 765
 Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
 770 775 780
 Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
 785 790 795 800
 Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
 805 810 815
 Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
 820 825 830
 Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
 835 840 845

<210> 32
 <211> 845
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:hybrid
 polymerase PhS2 from Figure 11

<400> 32
 Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
 1 5 10 15
 Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
 20 25 30
 Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
 35 40 45
 Asp Glu Val Arg Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Ile Asp Ala Glu Lys Val Arg Lys Lys Phe Leu Gly Lys Pro Ile
 65 70 75 80
 Glu Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
 85 90 95
 Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
 100 105 110
 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125
 Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
 130 135 140
 Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
 145 150 155 160
 Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
 165 170 175
 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
 180 185 190
 Arg Phe Leu Lys Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
 195 200 205
 Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
 210 215 220
 Lys Leu Gly Ile Lys Leu Pro Ile Gly Arg Asp Gly Ser Glu Pro Lys
 225 230 235 240
 Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
 245 250 255
 His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
 260 265 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
275 280 285
Lys Val Tyr Ala His Glu Ile Ala Glu Ala Trp Glu Ser Gly Glu Gly
290 295 300
Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305 310 315 320
Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ile Gln Leu Ser Arg Leu
325 330 335
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340 345 350
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
355 360 365
Pro Asn Lys Pro Ser Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
370 375 380
Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385 390 395 400
Ile Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
405 410 415
His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Glu Tyr
420 425 430
Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
435 440 445
Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
450 455 460
Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Ile Leu Leu
465 470 475 480
Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
485 490 495
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
500 505 510
Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Leu Val Arg Lys Glu
515 520 525
Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
530 535 540
Leu Tyr Ala Thr Ile Pro Gly Gly Lys Ser Glu Glu Ile Lys Lys Lys
545 550 555 560
Ala Leu Glu Phe Val Asp Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
565 570 575
Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
580 585 590

Lys Arg Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
 595 600 605
 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Lys Val Leu Glu Thr Ile Leu Lys His Gly Asn Val Glu Glu Ala
 625 630 635 640
 Val Arg Ile Val Lys Glu Val Thr Gln Lys Leu Ala Lys Tyr Glu Ile
 645 650 655
 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Pro Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
 675 680 685
 Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Tyr Gln Lys Thr Lys Gln Val Asp Leu Thr Ala
 755 760 765
 Cys Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
 770 775 780
 Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
 785 790 795 800
 Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
 805 810 815
 Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
 820 825 830
 Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
 835 840 845

<210> 33
 <211> 145
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:hybrid
 polymerase PhS3 from Figure 11

<400> 33
 Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Ile Ile
 1 5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Val Glu Tyr Asp Arg
 20 25 30
 Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
 35 40 45
 Asp Glu Val Arg Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
 65 70 75 80
 Glu Val Trp Lys Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
 85 90 95
 Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
 100 105 110
 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125
 Met Glu Gly Val Arg Tyr Arg Asn Pro Leu Ser Arg Arg Arg Arg Val
 130 135 140
 Trp
 145

<210> 34
 <211> 844
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:hybrid
 polymerase PhS4 from Figure 11

<400> 34
 Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
 1 5 10 15
 Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
 20 25 30
 Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile
 35 40 45
 Asp Glu Val Arg Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
 65 70 75 80
 Glu Val Trp Lys Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Ala Ile
 85 90 95
 Arg Glu Lys Val Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
 100 105 110
 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125

Phe	Ile	Pro	Ser	Leu	Leu	Lys	His	Leu	Leu	Asp	Glu	Arg	Gln	Lys	Ile	450	455	460
Lys	Arg	Lys	Met	Lys	Glu	Ser	Gln	Asp	Pro	Ile	Glu	Lys	Lys	Met	Leu	465	470	475
Asp	Tyr	Arg	Gln	Arg	Ala	Ile	Lys	Leu	Leu	Ala	Asn	Ser	Tyr	Tyr	Gly	485	490	495
Tyr	Tyr	Gly	Tyr	Ala	Lys	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Cys	Ala	Glu	500	505	510
Ser	Val	Thr	Ala	Trp	Gly	Arg	Glu	Tyr	Ile	Glu	Phe	Val	Arg	Lys	Glu	515	520	525
Leu	Glu	Glu	Lys	Phe	Gly	Phe	Lys	Val	Leu	Tyr	Ile	Asp	Thr	Gly	Leu	530	535	540
Tyr	Ala	Thr	Ile	Pro	Gly	Ala	Lys	Ser	Glu	Glu	Ile	Lys	Lys	Lys	Ala	545	550	555
Leu	Glu	Phe	Val	Lys	Tyr	Ile	Asn	Ser	Lys	Leu	Pro	Gly	Leu	Leu	Glu	565	570	575
Leu	Glu	Tyr	Glu	Gly	Phe	Tyr	Val	Arg	Gly	Phe	Phe	Val	Thr	Lys	Lys	580	585	590
Arg	Tyr	Ala	Leu	Ile	Asp	Glu	Glu	Gly	Lys	Ile	Ile	Thr	Arg	Gly	Leu	595	600	605
Glu	Ile	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	Thr	Gln	Ala	610	615	620
Arg	Val	Leu	Glu	Thr	Ile	Leu	Lys	His	Gly	Asn	Val	Glu	Glu	Ala	Val	625	630	635
Arg	Ile	Val	Lys	Glu	Val	Thr	Lys	Lys	Leu	Ser	Asn	Tyr	Glu	Ile	Pro	645	650	655
Pro	Glu	Lys	Leu	Ala	Ile	Tyr	Glu	Gln	Ile	Thr	Arg	Pro	Leu	His	Glu	660	665	670
Tyr	Lys	Ala	Ile	Gly	Pro	His	Val	Ala	Val	Ala	Lys	Arg	Leu	Ala	Ala	675	680	685
Lys	Gly	Val	Lys	Ile	Arg	Pro	Gly	Met	Val	Ile	Gly	Tyr	Ile	Val	Leu	690	695	700
Arg	Gly	Asp	Gly	Pro	Ile	Ser	Asn	Arg	Ala	Ile	Leu	Ala	Glu	Glu	Tyr	705	710	715
Asp	Pro	Lys	Lys	His	Lys	Tyr	Asp	Ala	Glu	Tyr	Tyr	Ile	Glu	Asn	Gln	725	730	735
Val	Leu	Pro	Ala	Val	Leu	Arg	Ile	Leu	Glu	Ala	Phe	Gly	Tyr	Arg	Lys	740	745	750
Glu	Asp	Leu	Arg	Trp	Gln	Lys	Thr	Lys	Gln	Val	Gly	Leu	Thr	Ala	Trp	755	760	765

Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val Lys
 770 775 780
 Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile Lys
 785 790 795 800
 Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu Gly
 805 810 815
 Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro Lys
 820 825 830
 Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
 835 840

<210> 35
 <211> 845
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:hybrid
 polymerase PhS5 from Figure 11

<400> 35
 Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile
 1 5 10 15
 Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
 20 25 30
 Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile
 35 40 45
 Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
 65 70 75 80
 Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
 85 90 95
 Arg Asp Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
 100 105 110
 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125
 Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
 130 135 140
 Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
 145 150 155 160
 Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
 165 170 175
 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
 180 185 190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
 195 200 205
 Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
 210 215 220
 Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
 225 230 235 240
 Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile
 245 250 255
 His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
 260 265 270
 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
 275 280 285
 Lys Val Tyr Ala Asp Glu Ile Ala Glu Ala Trp Glu Ser Gly Lys Asn
 290 295 300
 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
 305 310 315 320
 Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
 325 330 335
 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
 340 345 350
 Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
 355 360 365
 Pro Asn Lys Pro Asp Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser
 370 375 380
 Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
 385 390 395 400
 Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
 405 410 415
 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu Tyr
 420 425 430
 Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
 435 440 445
 Phe Ile Pro Ser Leu Leu Lys His Leu Leu Asp Glu Arg Gln Glu Ile
 450 455 460
 Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Lys Met Leu
 465 470 475 480
 Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
 485 490 495
 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
 500 505 510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Leu Val Trp Lys Glu
 515 520 525
 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
 530 535 540
 Leu Tyr Ala Thr Ile Pro Gly Gly Lys Pro Glu Glu Ile Lys Lys Lys
 545 550 555 560
 Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
 565 570 575
 Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys
 580 585 590
 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
 595 600 605
 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Arg Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
 625 630 635 640
 Val Lys Ile Val Lys Glu Val Thr Gln Lys Leu Ala Lys Tyr Glu Ile
 645 650 655
 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
 675 680 685
 Ala Arg Gly Val Lys Val Arg Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Val Gly Leu Thr Ser
 755 760 765
 Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
 770 775 780
 Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
 785 790 795 800
 Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
 805 810 815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
820 825 830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
835 840 845

<210> 36

<211> 472

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid
polymerase PhS6 from Figure 11

<400> 36

Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile
1 5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
20 25 30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile
35 40 45

Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
50 55 60

Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65 70 75 80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
85 90 95

Arg Asp Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115 120 125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145 150 155 160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
180 185 190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
195 200 205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
210 215 220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225 230 235 240

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile
 35 40 45
 Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
 65 70 75 80
 Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
 85 90 95
 Arg Asp Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
 100 105 110
 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125
 Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
 130 135 140
 Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
 145 150 155 160
 Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
 165 170 175
 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
 180 185 190
 Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
 195 200 205
 Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
 210 215 220
 Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
 225 230 235 240
 Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile
 245 250 255
 His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
 260 265 270
 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
 275 280 285
 Lys Val Tyr Ala Asp Glu Ile Ala Glu Ala Trp Glu Ser Gly Lys Asn
 290 295 300
 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
 305 310 315 320
 Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
 325 330 335
 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
 340 345 350

Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
355 360 365
Pro Asn Lys Pro Asp Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser
370 375 380
Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385 390 395 400
Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
405 410 415
His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Asn Tyr
420 425 430
Asp Val Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
435 440 445
Phe Ile Pro Ser Leu Leu Gly Arg Leu Leu Glu Glu Arg Gln Glu Ile
450 455 460
Lys Thr Lys Met Lys Ala Thr Lys Asp Pro Ile Glu Lys Lys Leu Leu
465 470 475 480
Asp Tyr Arg Gln Lys Ala Ile Lys Ile Leu Ala Asn Ser Phe Tyr Gly
485 490 495
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
500 505 510
Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Phe Val Arg Lys Glu
515 520 525
Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
530 535 540
Leu Tyr Ala Thr Ile Pro Gly Gly Lys Pro Glu Glu Ile Lys Lys Lys
545 550 555 560
Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
565 570 575
Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys
580 585 590
Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
595 600 605
Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
610 615 620
Ala Arg Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625 630 635 640
Val Lys Ile Val Lys Glu Val Thr Gln Lys Leu Ala Lys Tyr Glu Ile
645 650 655
Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
660 665 670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
 675 680 685
 Ala Arg Gly Val Lys Val Arg Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Val Gly Leu Thr Ser
 755 760 765
 Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Glu Ala Thr Val
 770 775 780
 Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
 785 790 795 800
 Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
 805 810 815
 Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
 820 825 830
 Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
 835 840

<210> 38
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:6-His
 polyhistidine epitope tag, metal chelate affinity
 ligand

<400> 38
 His His His His His
 1 5

<210> 39
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:anti-DYKDDDDK
 epitope tag

<400> 39
 Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 40
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Fwd 1 PCR
 primer oligonucleotide

 <400> 40
 ttggtaccaa gttcatatg a 21

 <210> 41
 <211> 51
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Fwd 2 PCR
 primer oligonucleotide

 <400> 41
 ccgctgccga sctatgcgac cyctcacagc kcaggcctgg atctgcgtgc g 51

 <210> 42
 <211> 69
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Fwd 3 PCR
 primer oligonucleotide

 <400> 42
 ttccgaccgg tctgatcmmt sawattscgg awggttmtgm ggsgcagrtg ckgccgcgta 60
 gcggcctgg 69

 <210> 43
 <211> 98
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Fwd 4 PCR
 primer oligonucleotide

 <400> 43
 ttttgatcga trscgattat crgggcsaas tgawgrttak cstggtgaac ckgggcmasg 60
 awgaakttry gattsagcsg ggcgaacgta ttgcgcag 98

 <210> 44
 <211> 56
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Fwd 5 PCR
 primer oligonucleotide

<400> 44
 cgtggcgaag gcggttttgg ctctascggc asamaagtaat gaggatccga attctt 56

<210> 45
 <211> 89
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Rev A PCR
 primer oligonucleotide

<400> 45
 ggtcgcatag stcggcagcg gwaawtcttk gscatgasgc rgacgcwkaa ttttcasawy 60
 aaytttkytc atatgaagct tggtagcaa 89

<210> 46
 <211> 83
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Rev B PCR
 primer oligonucleotide

<400> 46
 gatcagaccg gtcggaayca gcrycstwtc ammcggckya akttycascg swtystyaak 60
 gsmcgcacgc agatccaggc ctg 83

<210> 47
 <211> 68
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Rev C PCR
 primer oligonucleotide

<400> 47
 ttttatcgat crkgcccrsc gcgttcagca scrytawgcc mtktttccag sccaggccgc 60
 tacgcggc 68

<210> 48
 <211> 107
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Rev D PCR
 primer oligonucleotide

<400> 48
tagagccaaa gccgccttcg ccacgmtsgg tctgagaaam wtcttccacc wsawyaamtt 60
ccrcygcws caccggcrca awaaycakct gcgcaatacg ttcgccc 107

<210> 49
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Rev D PCR
primer oligonucleotide

<400> 49
aagaattcgg atcctcatta ct 22

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer to
measure exonuclease activity

<220>
<221> modified_base
<222> (1)
<223> n = t modified by 6-carboxy-fluorescein (FAM)

<220>
<221> modified_base
<222> (45)
<223> n = t amino-linked to quencher
4-(4-dimethylaminophenylazo)benzoyl group (dabcyl,
DAB)

<400> 50
ntttttgagg tgtgtcctac acagcggagt gtaggacaca cctcn 45